



PubMed	Nucleotide	Protein	Genome	Structure	PopSet	Taxonomy	OMIM
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Limits		Index	History		Clipboard		
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1: P54967 BIOTIN SYNTHASE BLink, PubMed, Related Sequences, Taxonomy, LinkOut
(BIOTIN SYNTHETASE)

LOCUS BIOB_ARATH 378 aa PLN 01-OCT-2000
 DEFINITION BIOTIN SYNTHASE (BIOTIN SYNTHETASE).
 ACCESSION P54967
 PID g1705463
 VERSION P54967 GI:1705463
 DBSOURCE swissprot: locus BIOB_ARATH, accession P54967;
 class: standard.
 created: Oct 1, 1996.
 sequence updated: Oct 1, 1996.
 annotation updated: Oct 1, 2000.
 xrefs: gi: gi: 1045315, gi: gi: 1045316, gi: gi: 1403661, gi: gi: 1403662, gi: gi: 1769456, gi: gi: 1769457, gi: gi: 6598343, gi: gi: 2288983
 xrefs (non-sequence databases): InterPro IPR002684, Pfam PF01792
 KEYWORDS Biotin biosynthesis; Iron-sulfur; Transferase.
 SOURCE thale cress.
 ORGANISM *Arabidopsis thaliana*
 Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
 REFERENCE 1 (residues 1 to 378)
 AUTHORS Weaver,L.M., Yu,F., Wurtele,E.S. and Nikolau,B.J.
 TITLE Characterization of the cDNA and gene coding for the biotin synthase of *Arabidopsis thaliana*
 JOURNAL Plant Physiol. 110 (3), 1021-1028 (1996)
 MEDLINE 96417082
 REMARK SEQUENCE FROM N.A.
 STRAIN=CV. LANDSBERG ERECTA
 REFERENCE 2 (residues 1 to 378)
 AUTHORS Patton,D., Pacella,M. and Ward,E.
 TITLE Direct Submission
 JOURNAL Submitted (??-JUL-1996)
 REMARK SEQUENCE FROM N.A.
 STRAIN=CV. COLUMBIA; TISSUE=Leaf
 REFERENCE 3 (residues 1 to 378)
 AUTHORS Baldet,P. and Ruffet,M.L.
 TITLE Biotin synthesis in higher plants: isolation of a cDNA encoding *Arabidopsis thaliana* bioB-gene product equivalent by functional complementation of a biotin auxotroph mutant bioB105 of *Escherichia coli* K12
 JOURNAL C. R. Acad. Sci. III, Sci. Vie 319 (2), 99-106 (1996)
 MEDLINE 96307524
 REMARK SEQUENCE FROM N.A.
 STRAIN=CV. COLUMBIA; TISSUE=Leaf
 REFERENCE 4 (residues 1 to 378)
 AUTHORS Lin,X., Kaul,S., Rounsley,S.D., Shea,T.P., Benito,M.-I., Town,C.D., Fujii,C.Y., Mason,T.M., Bowman,C.L., Barnstead,M.E., Feldblyum,T.V., Buell,C.R., Ketchum,K.A., Lee,J.J., Ronning,C.M., Koo,H., Moffat,K.S., Cronin,L.A., Shen,M., VanAken,S.E., Umayam,L., Tallon,L.J., Gill,J.E., Adams,M.D., Carrera,A.J., Creasy,T.H.,

Goodman,H.M., Somerville,C.R., Copenhaver,G.P., Preuss,D.,
Nierman,W.C., White,O., Eisen,J.A., Salzberg,S.L., Fraser,C.M. and
Venter,J.C.

TITLE Sequence and analysis of chromosome 2 of the plant *Arabidopsis thaliana*

JOURNAL Nature 402 (6763), 761-768 (1999)

MEDLINE 20083487

REMARK SEQUENCE FROM N.A.

STRAIN=CV. COLUMBIA

COMMENT

This SWISS-PROT entry is copyright. It is produced through a
collaboration between the Swiss Institute of Bioinformatics and
the EMBL outstation - the European Bioinformatics Institute.
The original entry is available from <http://www.expasy.ch/sprot>
and <http://www.ebi.ac.uk/sprot>

[CATALYTIC ACTIVITY] DETHIOBIOTIN + (S) = BIOTIN.

[PATHWAY] LAST STEP IN BIOTIN BIOSYNTHESIS PATHWAY.

[SIMILARITY] BELONGS TO THE BIOTIN AND LIPOIC ACID SYNTHETASES
FAMILY.

FEATURES

	Location/Qualifiers
source	1..378 /organism="Arabidopsis thaliana" /db_xref="taxon:3702"
Protein	1..378 /product="BIOTIN SYNTHASE" /EC_number="2.8.1.6"
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Site	98 /site_type="metal-binding" /note="IRON-SULFUR (POTENTIAL)."
Site	101 /site_type="metal-binding" /note="IRON-SULFUR (POTENTIAL)."

ORIGIN

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61 lldllfhgaq vhrhvhnfre vqqctllsik tggcsedcsy cpqssrystg vkaqrlmskd
121 avidaakkak eagstrfcmg aawrdtigrk tnfsqileyi keirgmgmev cctlgmiekq
181 qalelkkagl taynhnldts reyyppnvitt rsyddrletl shvrdaginv csggiiglge
241 aeedrigllh tlatlpshpe svpinallav kgtpledqkp veiwemirmi gtarivmpka
301 mvrlsagrvr fsmseqalcf lagansiftg eklttpnnd fdadqlmfkt lglipkppsf
361 seddsesenc ekvasash

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Protein

PubMed	Nucleotide	Protein	Genome	Structure	PopSet	Taxonomy	OMIM
Search		Protein	Limits		Index	History	Clipboard
Display		Default View	as	HTML	Save	Add to Clipboard	

1: CAA18303 **biotin synthase (EC 2.8.1.6)** [Schizosaccharomyces pombe] BLink, Related Sequences, Nucleotide, Taxonomy

LOCUS CAA18303 363 aa PLN 06-APR-1999
 DEFINITION biotin synthase (EC 2.8.1.6) [Schizosaccharomyces pombe].
 ACCESSION CAA18303
 PID g2995363
 VERSION CAA18303.1 GI:2995363
 DBSOURCE embl locus SPCC320, accession AL022245.2
 KEYWORDS
 SOURCE fission yeast.
 ORGANISM Schizosaccharomyces pombe
 Eukaryota; Fungi; Ascomycota; Schizosaccharomycetales;
 Schizosaccharomycetaceae; Schizosaccharomyces.
 REFERENCE 1 (residues 1 to 363)
 AUTHORS Wood, V., Rajandream, M.A., Barrell, B.G., Wedler, H., Wambutt, R. and Wedler, E.
 TITLE Direct Submission
 JOURNAL Submitted (24-MAR-1998) European Schizosaccharomyces genome sequencing project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton, Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and AGOWA GmbH, Glienicke Weg 185, D-12489 Berlin, Germany
 COMMENT Notes:
 Protein coding regions (CDS) have been predicted with the help of computer analysis using the Genefinder program in PomBase (an ACEDB database) with additional predictions for the branch-acceptor sites supplied by the program Sp3splice. CAUTION: It is possible that for any individual CDS we may have underestimated or overestimated the number of introns/exons or we may not have chosen the correct splice donor/acceptor sites. CDS are numbered using the following system eg SPBC25H2.01c. SP (S. pombe), B (chromosome 2), c25H2 (cosmid name), .01 (first CDS), c (complementary strand).
 The more significant matches with motifs in the PROSITE database are also included but some of these may be fortuitous. The length in codons is given for each CDS.
 IMPORTANT: This sequence MAY NOT be the entire insert of the sequenced clone. It may be shorter because we only sequence overlapping sections once, or longer, because we arrange for a small overlap between neighbouring submissions. Details of yeast sequencing at the Sanger Centre are available on the World Wide Web.
 (URL, http://www.sanger.ac.uk/Projects/S_pombe/)
 During 1995 to 1996 about 66% of S. pombe chromosome 1 was sequenced by the Sanger Centre. The sequencing of the S. pombe genome is now being continued with funding from The European Commission. Fourteen European sequencing laboratories, including the Sanger Centre, are participating in the project.
 Cosmid c320 is overlapped by cosmid c330 at the 5' end and c1235 at the 3' end.
 FEATURES Location/Qualifiers
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Protein 1..363
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CDS 1..363
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    /label=bio2
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    /note="SPCC320.01c, len:362"
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61 llsiktggct edckycqss ryntgvkatk lmkidevlek akiakakgst rfcmgawrd
121 lngnrntfkn ileiikevrs mdmevcvtlg mlneqqakel kdagltaynh nldtsreyys
181 kiistrtyde rln tidnlrk aglkvcsggi lglgekkhdr vglihslatm pthpesvpfn
241 llvpipgtpv gdavkerlpi hpflrsiata ricmpktiir faagrntcse seqalafmag
301 anavftgekm lttpavswds dsqlyfynwgl egmqsfeygt stegedgtft lppkerlaps
361 psl
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PubMed	Nucleotide	Protein	Genome	Structure	PopSet	Taxonomy	OMIM
Search	Protein	<input type="checkbox"/> for					
Limits		Index	History	Clipboard			
Display	Default View	<input type="checkbox"/> as	HTML	<input type="checkbox"/> Save	Add to Clipboard		

1: NP_011802 Biotin synthase; BLink, PubMed, Related Sequences, Nucleotide, Genome, T
 Bio2p
 [Saccharomyces
 cerevisiae]

LOCUS NP_011802 375 aa PLN 30-JAN-2001
 DEFINITION Biotin synthase; Bio2p [Saccharomyces cerevisiae].
 ACCESSION NP_011802
 PID g6321725
 VERSION NP_011802.1 GI:6321725
 DBSOURCE REFSEQ: accession NC_001139.1
 KEYWORDS .
 SOURCE baker's yeast.
 ORGANISM Saccharomyces cerevisiae
 Eukaryota; Fungi; Ascomycota; Saccharomycetes; Saccharomycetales;
 Saccharomycetaceae; Saccharomyces.
 REFERENCE 1 (residues 1 to 375)
 AUTHORS Goffeau,A., Barrell,B.G., Bussey,H., Davis,R.W., Dujon,B.,
 Feldmann,H., Galibert,F., Hoheisel,J.D., Jacq,C., Johnston,M.,
 Louis,E.J., Mewes,H.W., Murakami,Y., Philippsen,P., Tettelin,H. and
 Oliver,S.G.
 TITLE Life with 6000 genes
 JOURNAL Science 274 (5287), 546 (1996)
 MEDLINE 97002444
 REFERENCE 2 (residues 1 to 375)
 AUTHORS Tettelin,H., Agostoni Carbone,M.L., Albermann,K., Albers,M.,
 Arroyo,J., Backes,U., Barreiros,T., Bertani,I., Bjourson,A.J.,
 Bruckner,M., Bruschi,C.V., Carignani,G., Castagnoli,L., Cerdan,E.,
 Clemente,M.L., Coblentz,A., Coglievina,M., Coissac,E., Defoor,E.,
 Del Bino,S., Delius,H., Delneri,D., de Wergifosse,P., Dujon,B.,
 Kleine,K. et al.
 TITLE The nucleotide sequence of Saccharomyces cerevisiae chromosome VII
 JOURNAL Nature 387 (6632 Suppl), 81-84 (1997)
 MEDLINE 97313265
 REFERENCE 3 (residues 1 to 375)
 AUTHORS Saccharomyces Genome Database (yeast-curator@genome.stanford.edu).
 TITLE Direct Submission
 JOURNAL Submitted (17-NOV-1999) Department of Genetics, Stanford
 University, Saccharomyces Genome Database, Stanford, CA 94305-5120,
 USA
 COMMENT REFSEQ: This reference sequence was provided by the Saccharomyces
 Genome Database (SGD).
 Method: conceptual translation.
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 /strain="S288C"
 /db_xref="taxon:4932"
 /chromosome="VII"
 Protein 1..375
 /product="Biotin synthase"
 /note="Bio2p"
 CDS 1..375
 /gene="BIO2"

/db_xref="SGD:S0003518"

/coded_by="complement(NC_001139.1:1063809..1064936)"

ORIGIN

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61 iyhtpllelt haaqlqhrkw hdptkvqlct lmniksggcs edckycqss rndtglkaek
121 mvkvdevike aeeakrngst rfclgaawrd mkgrksamkr iqemvkvnd mgletcvtlg
181 mvdqdaqql kdagltaynh nidtsrehys kvitttrtydd rlqtiknvqe sgikactggi
241 lglgeseddh igfiytlslm sphpeslpin rlvaikgtpm aeeladpsk klqfdeilrt
301 iatarivmpk aiirlaagry tmketeqfvc fmagcnsift gkkmlttmcn gwdedkamla
361 kwglqpmeaf kydrs
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